

Sequence Listing could not be accepted due to errors.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2011; month=3; day=28; hr=11; min=18; sec=10; ms=496;]

Reviewer Comments:

 $\langle 400 \rangle$ 1

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala

1 5 10 15

Please correct the misaligned amino acid codings in the above Sequence ID# 1, found at locations 1 through 15.

Application No: 10556853 Version No: 3.0

Input Set:

Output Set:

Started: 2011-03-10 10:31:27.859
Finished: 2011-03-10 10:31:28.300
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 441 ms
Total Warnings: 0
Total Errors: 4
No. of SeqIDs Defined: 1
Actual SeqID Count: 1

Error code	Error Description
E 323	Invalid/missing amino acid numbering SEQID (1) POS (9)
E 323	Invalid/missing amino acid numbering SEQID (1)at Protein (10)
E 323	Invalid/missing amino acid numbering SEQID (1) POS (14)
E 323	Invalid/missing amino acid numbering SEQID (1)at Protein (15)

SEQUENCE LISTING

<110> GNJATIC, Sacha
 ATANACKOVIC, Djordje
 OLD, Lloyd J.

<120> Isolated NY-ESO-1 Peptides Which Bind to HLA Class II Molecules
 and Uses Thereof

<130> LUD 5826 US

<140> 10556853

<141> 2011-03-10

<150> PCT/US04/16849

<151> 2004-05-27

<150> 60/474,893

<151> 2003-05-30

<160> 1

<170> PatentIn version 3.2

<210> 1

<211> 180

<212> PRT

<213> Homo sapiens

<400> 1

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala
 1 5 10 15

Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn
 20 25 30

Ala Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Ala Pro
 35 40 45

Arg Gly Ala Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala
 50 55 60

Pro Arg Gly Pro His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys
 65 70 75

Cys Arg Cys Gly Ala Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe
 80 85 90

Tyr Leu Ala Met Pro Phe Ala Thr Pro Met Glu Ala Glu Leu Ala
 95 100 105

Arg Arg Ser Leu Ala Gln Asp Ala Pro Pro Leu Pro Val Pro Gly
 110 115 120

Val Leu Leu Lys Glu Phe Thr Val Ser Gly Asn Ile Leu Thr Ile

125	130	135
Arg Leu Thr Ala Ala Asp His Arg Gln Leu Gln Leu Ser Ile Ser		
140	145	150
Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp Ile Thr Gln Cys		
155	160	165
Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly Gln Arg Arg		
170	175	180